

Sullivan, Daniel

From: Sullivan, Daniel
Sent: Tuesday, September 27, 2005 7:56 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search 09/982091

Please search for the following in the pending, issued patent and commercial databases:

A nucleic acid encoding SEQ ID NO: 4;
A nucleic acid encoding SEQ ID NO: 2;
A nucleic acid comprising residues 1-500 of SEQ ID NO: 1;
A nucleic acid comprising residues 4200-4740 of SEQ ID NO: 1;
A nucleic acid comprising residues 1-500 of SEQ ID NO: 5;
A nucleic acid comprising residues 58300-58837 of SEQ ID NO: 5

Thank you.

Daniel M. Sullivan

Examiner AU 1636
Remsen Bldg.
Room 2A74

Tel: (571) 272-0779

Mailbox: 2C70

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: October 3, 2005, 21:21:46 ; Search time 1847.42 Seconds
(without alignments)
14110.995 Million cell updates/sec

Title: US-09-982-091a-5_COPY_58300_58837

Perfect score: 538

Sequence: 1 caggtgacagagagagagca.....tatgcacagcagctccctgag 538

Scoring table: IDENTITY NTC

Gapop 10_0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pri:*
10: gb_pro:*
11: gb_sce:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538	100.0	194296	9	ALJ34864 Human DNA
2	361	67.1	2567	9	BC026909 Homo sapi
3	361	67.1	2615	6	AR338531 Sequence
4	361	67.1	2934	6	AK834078 Sequence
5	361	67.1	2934	6	AK096303 Homo sapi
6	356	66.2	1046	6	CQ727306 Sequence
7	300.2	55.8	2394	6	AX834179 Sequence
8	300.2	55.8	2394	9	AK096466 Homo sapi
9	255.2	47.4	213391	10	AL606935
10	242	45.0	223363	2	AC120700
11	242	45.0	247462	2	AC134478
12	227	42.2	203980	2	AC134478 Rattus no
13	51.6	9.6	125020	9	AF429315 Homo sapi
14	43	8.0	125020	9	AF429315 Homo sapi
15	39	7.2	364	6	AR425705 Sequence
16	39	7.2	364	6	AR425705 Sequence
17	39	7.2	364	6	BD121258 EST and e
18	38.2	7.1	210813	10	AL627070 Mouse DNA
19	37.8	7.0	135851	9	AC091714 Papio anu

20	37.6	7.0	212050	1	AL646060	Al646060 Ralstonia
21	37.4	7.0	415	6	CQ451255	CQ451255 Sequence
22	37.4	7.0	1605	6	BD180291	BD180291 Highly th
23	37.4	7.0	25593	3	CEH21P03	295619 Caenorhabdi
24	37.4	7.0	144734	2	AC148922	AC148922 Dasyatis n
25	37.4	7.0	179439	2	AC131897	AC131897 Oryctolag
26	37.4	7.0	211730	10	AC132621	AC132621 Mus muscu
27	37.4	7.0	252686	2	AC126177	AC126177 Rattus no
28	37.4	7.0	265229	2	AC121468	AC121468 Rattus no
29	37.4	7.0	274676	1	AE017305	AE017305 Thermus t
30	37.2	6.9	3120	6	CQ717965	CQ717965 Homo sapien
31	37.2	6.9	3120	6	HSU58917	HSU58917 Homo sapien
32	37.2	6.9	3223	6	AR034066	AR034066 Sequence
33	37.2	6.9	3223	6	AR097753	AR097753 Sequence
34	37.2	6.9	3223	6	AR102359	AR102359 Sequence
35	37.2	6.9	3223	6	AR104870	AR104870 Sequence
36	37.2	6.9	3223	6	AR131081	AR131081 Sequence
37	37.2	6.9	3223	6	AR137603	AR137603 Sequence
38	37.2	6.9	3223	6	AR453137	AR453137 Sequence
39	37.2	6.9	3223	6	BD023246	BD023246 Method fo
40	37.2	6.9	3373	9	BC011624	BC011624 Homo sapi
41	37.2	6.9	51574	2	AC138651	AC138651 Homo sapi
42	37.2	6.9	82806	9	AC007111	AC007111 Homo sapi
43	37.2	6.9	101269	9	AC005300	AC005300 Homo sapi
44	37.2	6.9	149061	9	AC098805	AC098805 Homo sapi
45	37.2	6.9	149061	9	AC098805	AC098805 Homo sapi

ALIGNMENTS

RESULT 1
ALJ34864
LOCUS
DEFINITION
Human DNA sequence from clone RP11-435D7 on chromosome 1. Contains ESTs, STSs, GSSs and Cpg islands. Contains a novel gene and the 5' part of the PSMB2 gene for proteasome (prosome, macropain) subunit 2, beta type, complete sequence.

ACCESSION
ALJ34864.16 GI:10185566
VERSION
HTG; Cpg Island; macropain; prosome; proteasome; PSMB2.
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 194296)
AUTHORS
Howden, P.
JOURNAL
Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgeshire, UK.
COMMENT
Direct Submission
requesters: clonerequest@sanger.ac.uk
On Sep 19, 2000 this sequence version replaced gi:9714820.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence is the entire insert of clone RP11-435D7 The true left end of clone RP11-435D7 is at 123829 in this sequence. The true right end of clone RP11-435D7 is at 81044 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 21:21:46 ; Search time 1716.93 seconds
(without alignments)
1410.995 Million cell updates/sec

Title: US-09-982-091a-5_COPY_1_500

Perfect score: 500
Sequence: 1 aagcagcagcttcttaactc.....tgcacccagcgcgagctgc 500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_nlg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_stra:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	500	100.0	194296	9	AL354864 Human DNA
2	498.4	99.7	118862	2	AL133143 Homo sapi
3	61.8	12.4	87307	9	AC133791 Homo sapi
4	61.8	12.4	132899	9	AC093506 Homo sapi
5	61.8	12.4	153225	9	AC013581 Homo sapi
6	61.8	12.4	153538	9	AC093279 Homo sapi
7	61.8	12.4	174039	9	AC138853 Homo sapi
8	61.8	12.4	186972	9	AC137794 Homo sapi
9	61.8	12.4	189670	2	AC041047 Homo sapi
10	61.8	12.4	190684	2	AC139798 Homo sapi
11	61.8	12.4	193666	2	AC140124 Homo sapi
12	61.8	12.4	222307	2	AC140514 Homo sapi
13	60.4	12.1	159191	2	AC053535 Homo sapi
14	60.4	12.1	159112	9	AC040975 Homo sapi
15	59.8	12.0	155942	9	AC136691 Homo sapi
16	59.8	12.0	161765	9	AC113190 Homo sapi
17	59.8	12.0	176479	9	AC113631 Homo sapi
18	59.8	12.0	337344	6	CO869869 Sequence
19	59.2	11.8	144319	9	AC112218 Homo sapi

20	59.2	11.8	162997	9	AC092035 Homo sapi
21	58.8	11.8	172650	9	AC136968 Homo sapi
22	58.8	11.8	255818	2	AC145871 Pan trogl
23	58.4	11.7	41924	2	AC087403 Homo sapi
24	58.4	11.7	165459	9	AC090587 Homo sapi
25	58.4	11.7	173720	9	AC097264 Pan trogl
26	58.4	11.7	181835	9	AC091152 Homo sapi
27	58.4	11.7	184106	9	AC060812 Homo sapi
28	58	11.6	19751	2	AC048335 Homo sapi
29	58	11.6	17699	2	AC053518 Homo sapi
30	58	11.6	181445	9	AC026367 Homo sapi
31	57.8	11.6	67372	9	AL138741 Human DNA
32	57.2	11.4	143981	9	HSJ1050K3 Human DNA
33	57	11.4	108687	9	AL356320 Human DNA
34	57	11.4	128837	9	AL450304 Human DNA
35	56.8	11.4	119063	9	AC027311 Homo sapi
36	56.8	11.4	172239	2	AC079307 Homo sapi
37	56.6	11.3	628	6	BD275472 47 Human
38	56.6	11.3	80149	2	AC025995 Homo sapi
39	56.6	11.3	91654	9	AL357118 Human DNA
40	56.6	11.3	130027	9	AC004982 Homo sapi
41	56.6	11.3	148852	9	AC005878 Homo sapi
42	56.6	11.3	163652	2	AC145845 Pan trogl
43	56.6	11.3	165002	2	AL355814 Homo sapi
44	56.6	11.3	175020	9	AC024267 Homo sapi
45	56.6	11.3	177773	9	AC010761 Homo sapi

ALIGNMENTS

RESULT 1
AL354864
LOCUS
DEFINITION
AL354864 194296 bp DNA linear PRI 04-APR-2001
Human DNA sequence from clone RP11-435D7 on chromosome 1. Contains ESTs, STSs, GSSs and Cpg islands. Contains a novel gene and the 5' part of the PSMB2 gene for proteasome (prosome, macropain) subunit 2, beta type, complete sequence.

ACCESSION
AL354864
VERSION
AL354864.16 GI:10185566
HTG; Cpg island; macropain; prosome; proteasome; PSMB2.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgehire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
1 (bases 1 to 194296)

COMMENT
Direct Submission
Submitted (06-DEC-2000) Sanger Centre, Hinxton, Cambridgehire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Sep 19, 2000 this sequence version replaced gi:9714820.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submissions only a small overlap as described above.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>
This sequence is the entire insert of clone RP11-435D7 The true left end of clone RP1-62B3 is at 123829 in this sequence. The true right end of clone RP4-555P23 is at 81044 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known

No.	Score	Match	Length	DB	ID	Description
1	361	67.1	2615	4	US-09-630-312D-1720	Sequence 22, Appl
2	39	7.2	3264	4	US-08-621-976-17202	Sequence 11202, Appl
3	37.2	6.9	3223	4	US-08-620-694A-9	Sequence 9, Appl
4	37.2	6.9	3223	3	US-09-022-285-9	Sequence 9, Appl
5	37.2	6.9	3223	3	US-09-022-686-9	Sequence 9, Appl
6	37.2	6.9	3223	3	US-08-978-773-3	Sequence 3, Appl
7	37.2	6.9	3223	3	US-09-022-253-9	Sequence 3, Appl
8	37.2	6.9	3223	3	US-09-022-260-9	Sequence 9, Appl
9	37.2	6.9	3223	3	US-09-022-259-9	Sequence 9, Appl
10	37.2	6.9	3223	3	US-09-022-257-9	Sequence 9, Appl
11	37.2	6.9	3223	4	US-09-549-679-9	Sequence 9, Appl
12	37.2	6.9	16154	4	US-09-949-016-16669	Sequence 16669, Appl
13	36.4	6.8	8916	3	US-09-579-181-11	Sequence 11, Appl
14	36.4	6.8	9354	3	US-09-579-181-10	Sequence 10, Appl
15	35	6.5	3154	4	US-09-949-016-2101	Sequence 2101, Appl
16	34.8	6.5	63319	4	US-09-949-016-16579	Sequence 16579, Appl
17	34	6.3	771	2	US-08-972-008-3	Sequence 3, Appl
18	34	6.3	771	3	US-09-267-409-3	Sequence 3, Appl
19	34	6.3	1349	4	US-09-949-016-1391	Sequence 1391, Appl
20	34	6.3	1740	4	US-08-796-101-50	Sequence 50, Appl
21	34	6.3	2495	3	US-09-141-027-1	Sequence 1, Appl
22	34	6.3	2495	4	US-09-617-804-1	Sequence 1, Appl
23	34	6.3	2500	4	US-09-949-016-791	Sequence 791, Appl
24	34	6.3	2525	2	US-08-972-008-1	Sequence 1, Appl
25	34	6.3	2525	3	US-09-267-409-1	Sequence 1, Appl
26	33.8	6.3	1127	4	US-09-620-312D-254	Sequence 254, Appl
27	33.8	6.3	8310	3	US-08-870-126-11	Sequence 11, Appl

28	33.8	6.3	8310	3	US-09-44-655-247-11	Sequence 11, Appl
29	33.8	6.3	14985	1	US-08-652-972A-6	Sequence 6, Appl
30	33.8	6.3	21856	5	PCR-US96-06231A-6	Sequence 6, Appl
31	33.8	6.3	14985	4	US-09-949-016-11205	Sequence 12205, A
32	33.4	6.2	12300	4	US-09-799-451-18	Sequence 18, Appl
33	33.4	6.2	32010	4	US-09-949-016-1127	Sequence 1127, A
34	33.4	6.2	1230025	4	US-09-199-442A-1	Sequence 1, Appl
35	33.4	6.2	1230230	4	US-09-438-185A-1	Sequence 1, Appl
36	33.2	6.2	2549	3	US-09-467-082-3	Sequence 3, Appl
37	33.2	6.2	2549	4	US-09-394-455-5	Sequence 5, Appl
38	33.2	6.2	2549	4	US-09-949-016-3584	Sequence 3584, Ap
39	33.2	6.2	2608	4	US-09-394-455-35	Sequence 35, Appl
40	33.2	6.2	12425	4	US-09-616-289-50	Sequence 50, Appl
41	33.2	6.2	29930	4	US-09-949-016-15326	Sequence 15326, A
42	33	6.1	2831	2	US-08-808-982-3	Sequence 3, Appl
43	33	6.1	2831	3	US-09-306-902A-3	Sequence 3, Appl
44	32.8	6.1	981	4	US-09-252-991A-31673	Sequence 13673, A
45	32.8	6.1	1056	4	US-09-252-991A-13421	Sequence 13421, A

ALIGNMENTS

RESULT 1
US-09-620-312D-22

```

Sequence 22, Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyang
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aйдong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, ping
APPLICANT: Ma, Yungting
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhilwei
APPLICANT: John Tillinghaast
APPLICANT: Dermanac, Radoje T.
TITLE OF INVENTION: NO. 6569662el Nucleic Acids and
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_fl_genes Version 1.0
SEQ ID NO 22
LENGTH: 2615
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS (849)
LOCATION: (160)..(849)
US-09-620-312D-22

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Query Match: 67.1%; Score 361; DB 4; Length 2615;

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Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Dy 178 GCTAGATGTTCCGCCATCCAGCGCAGGGCTGACTGAGGGGGGCCAATTCTTGGGGGACCCAC 23
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 155 GCTAGATGTTCCGCCATCCAGCGCAGGGCTGACTGAGGGGGGCCAATTCTTGGGGGACCCAC 214

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 21:10:56 : Search time 278.963 seconds
(without alignments)
11416.644 Million cell updates/sec

Title: US-09-982-091a-5_COPY_58300_58837

Perfect score: 538
Sequence: 1 cagctagcagcagcgagcgagcga.....tatgcacgacgtccctcgag 538

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4330206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn19808:*
- 2: geneseqn19908:*
- 3: geneseqn20008:*
- 4: geneseqn20018:*
- 5: geneseqn20028:*
- 6: geneseqn20038:*
- 7: geneseqn20048:*
- 8: geneseqn20058:*
- 9: geneseqn20068:*
- 10: geneseqn20078:*
- 11: geneseqn20088:*
- 12: geneseqn20098:*
- 13: geneseqn20108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538	100.0	58837	6	ABK52612
2	361	67.1	2615	2	AA158146
3	361	67.1	2615	5	ADQ98352
4	361	67.1	2615	9	ADQ98352
5	361	67.1	2615	11	ADQ98352
6	359.4	66.8	2616	4	AA159932
7	300.2	55.8	2394	11	ADM02618
8	38	7.1	10902	5	AA690570
9	37.4	7.0	415	6	ABN24269
10	37.2	6.9	3120	10	ADD25545
11	37.2	6.9	3120	10	ADK61414
12	37.2	6.9	3120	12	ADP09696
13	37.2	6.9	3120	12	ADP13348
14	37.2	6.9	3223	2	AA733801
15	37.2	6.9	3223	2	AA727592
16	37.2	6.9	3223	2	AA701922
17	37.2	6.9	3223	3	AA51988
18	37.2	6.9	3223	3	AA52146
19	37.2	6.9	3223	3	AA59871
20	37.2	6.9	3223	3	AA61240

21	37.2	6.9	3223	4	AA57188	AA57188 Human IL-
22	37.2	6.9	3223	4	AA002815	AA002815 Human int
23	37.2	6.9	3223	12	ADJ88264	ADJ88264 Human IL-
24	37.2	6.9	3223	12	ADL24268	ADL24268 Human IL-
25	37.2	6.9	3223	12	ADQ91251	ADQ91251 Human CDN
26	37.2	6.9	3223	12	ADQ91307	ADQ91307 Human int
27	37.2	6.9	3429	10	ADG32974	ADG32974 Human int
28	36.4	6.8	2200	8	ADN71938	ADN71938 Human DNA
29	36.4	6.8	2244	8	AA590569	AA590569 Rice gene
30	36.4	6.8	5580	5	ABA82988	ABA82988 Human tta
31	36.4	6.8	7666	13	ADR07802	ADR07802 Full leng
32	36.4	6.8	8916	5	AA89860	AA89860 Human SRC
33	36.4	6.8	9126	10	ADG3126	ADG3126 Human bre
34	36.4	6.8	9354	5	AA89859	AA89859 Human SRC
35	36.4	6.8	9958	8	ACC46296	ACC46296 Human dlt
36	36.4	6.8	10795	3	AACT5440	AACT5440 Human dlt
37	36	6.7	5349	3	AAA5527	AAA5527 Porcine B
38	35.8	6.7	2895	12	AD010076	AD010076 Novel hum
39	35.4	6.6	1479	12	ADJ40245	ADJ40245 Plant CDN
40	35	6.5	34981	10	ADG87619	ADG87619 Human GPC
41	34.8	6.5	20015	5	ABA20740	ABA20740 Human ner
42	34.6	6.4	4348	5	AA545069	AA545069 CDNA enco
43	34.6	6.4	4401	10	ADP92402	ADP92402 Human ubi
44	34.6	6.4	4474	3	AACT6399	AACT6399 Human ORF
45	34.6	6.4	4506	12	ADL14063	ADL14063 Human CDN

ALIGNMENTS

RESULT 1
ID ABK52612 standard; DNA; 58837 BP.

XX ABK52612;

DT 27-AUG-2002 (first entry)

XX Human Claspin genomic sequence.

KW Chk1 protein; SQ/TQ motif; isoelectric point; cell cycle progression; ds;
nuclear localisation signal; DNA replication checkpoint; benign neoplasm;

KX cell proliferative disorder; malignant neoplasm; human; claspin.

XX Homo sapiens.

PN WO200233115-A2.

PD 25-APR-2002.

PF 17-OCT-2001; 2001WO-US032316.

PR 17-OCT-2000; 2000US-0241246P.

PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

PI Kumagai A, Dunphy WG;

DR WPI, 2002-454610/48.

PT Novel Claspin polypeptide specifically interacting with chk1 protein
useful for identifying compound that modulates cell cycle progression and

PT for treating cell proliferative disorder like neoplasm.

PS Claim 10; Fig 7; 97p; English.

CC The present invention relates to a new substantially pure Claspin
polypeptide that specifically interacts with a Chk1 protein, having SQ/TQ
motifs, an isoelectric point of 4.5 and at least one nuclear localisation
signal. The method of the invention is useful for identifying cell cycle
that modulates cell cycle progression and for modulating cell cycle
progression in a cell. The invention is useful for the proper operation
of DNA replication checkpoint in the cell cycle. The method is also

GenCore version 5.1.6
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OM nucleic acid - nucleic acid search, using SW model

Run on: October 4, 2005, 02:35:27 ; Search time 687.831 Seconds
(without alignments)
5019.154 Million cell updates/sec

Title: US-09-982-091A-5_COPY_1_500

Perfect score: 500

Sequence: 1 aagcaggtgagtttcaactt.....tgcacccagctgagtcg 500

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues 14885122

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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7	55.8	11.2	201	19	US-10-741-601-23976

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C	10	55.8	11.2	126872	19	US-10-741-601-5738	Sequence 5738, A
C	11	55.8	11.2	126872	21	US-10-741-600-17885	Sequence 17885, A
C	12	55.8	11.2	129722	19	US-10-450-826-24	Sequence 24, Appl
C	13	55.8	11.2	129722	20	US-10-723-860-844	Sequence 844, Appl
C	14	55.4	11.1	670	22	US-10-915-740A-210	Sequence 210, Appl
C	15	55.4	11.1	57038	22	US-10-287-436A-646	Sequence 646, Appl
C	16	55.4	11.1	92794	22	US-10-287-436A-708	Sequence 708, Appl
C	17	55	11.0	201	19	US-10-741-601-19945	Sequence 19945, A
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C	22	54.8	11.0	105499	19	US-10-332-261-326	Sequence 326, Appl
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C	26	54.4	10.9	1065	13	US-10-027-632-9476	Sequence 9476, Appl
C	27	54.4	10.9	1065	17	US-10-027-632-9474	Sequence 9474, Appl
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C	32	54	10.8	176001	17	US-10-210-556-37	Sequence 27, Appl
C	33	54	10.8	186739	17	US-10-210-556-19	Sequence 19, Appl
C	34	54	10.8	220224	13	US-10-087-182-1282	Sequence 1282, A
C	35	53.6	10.7	577	13	US-10-027-632-84682	Sequence 84682, A
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C	42	53.6	10.7	663	13	US-10-027-632-241851	Sequence 241851, A
C	43	53.6	10.7	663	17	US-10-027-632-241850	Sequence 241850, A
C	44	53.6	10.7	663	17	US-10-027-632-241851	Sequence 241851, A
C	45	53.6	10.7	347814	19	US-10-322-656-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1
US-09-982-091A-5
Sequence 5, Application US/09982091A
Patent No. US20020151030A1
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: KUMAGAI, AKIKO
APPLICANT: DUNPHY, WILLIAM
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
FILE REFERENCE: CIT1320-1
CURRENT APPLICATION NUMBER: US/09/982,091A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/241,246
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 58837
TYPE: DNA
ORGANISM: Homo sapiens
US-09-982-091A-5

Query Match 100.0%; Score 500; DB 9; Length 58837;
Best Local Similarity 100.0%; Pred. No. 8.2e-109; Indels 0; Gaps 0;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AAGCAGGTGTTTAACTTACTCCAGAGGAATAGCAGTAAATAATGTAACATGCTA 60

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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 00:01:51 : Search time 82.7321 Seconds
(without alignments)
9889.010 Million cell updates/sec

Title: US-09-982-091a-5_COPY_1_500

Perfect score: 500
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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	56.2	11.2	106256	US-09-949-016-16858	Sequence 16858, A
C 5	55.6	11.1	97376	US-09-949-016-16093	Sequence 16093, A
C 6	55.6	11.1	116966	US-09-949-016-17557	Sequence 17557, A
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C 8	55.2	11.0	475	US-09-949-016-155425	Sequence 155425, A
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C 10	54.6	10.9	601	US-09-949-016-63328	Sequence 63328, A
C 11	54.6	10.9	601	US-09-949-016-63329	Sequence 63329, A
C 12	54.6	10.9	63783	US-09-949-016-13576	Sequence 13576, A
C 13	54.6	10.9	237510	US-09-949-016-14273	Sequence 14273, A
C 14	54.4	10.9	601	US-09-949-016-108051	Sequence 108051, A
C 15	54.4	10.9	19990	US-09-949-016-14967	Sequence 14967, A
C 16	54.4	10.9	82000	US-09-949-016-15595	Sequence 15595, A
C 17	54.4	10.9	250352	US-09-949-016-14724	Sequence 14724, A
C 18	54.2	10.8	122626	US-09-949-016-17524	Sequence 17524, A
C 19	54	10.8	43192	US-09-949-016-15466	Sequence 15466, A
C 20	54	10.8	118923	US-09-949-016-13227	Sequence 13227, A
C 21	53.6	10.7	601	US-09-949-016-17756	Sequence 17756, A
C 22	53.6	10.7	601	US-09-949-016-17757	Sequence 17757, A
C 23	53.6	10.7	601	US-09-949-016-17758	Sequence 17758, A
C 24	53.6	10.7	601	US-09-949-016-17759	Sequence 17759, A
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C 26	53.6	10.7	110243	US-09-949-016-13698	Sequence 13698, A
C 27	53.6	10.7	150032	US-09-949-016-14321	Sequence 14321, A

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35	53.2	10.6	601	4	US-09-949-016-64065	Sequence 64065, A
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C 42	53	10.6	601	4	US-09-949-016-206135	Sequence 206135, A
C 43	53	10.6	601	4	US-09-949-016-206136	Sequence 206136, A
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C 45	53	10.6	14241	4	US-09-949-016-13869	Sequence 13869, A

ALIGNMENTS

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RESULT 1
US-09-949-016-191250/c
Sequence 191250, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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SEQ ID NO 191250
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-191250

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Best Local Similarity 66.9%; Pred. No. 3.3e-06;
Matches 83; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Sequence 17216, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 23:18:16 ; Search time 1645.02 Seconds
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11569.535 Million cell updates/sec

Title: US-09-982-091a-5_COPY_1_500

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Scoring table: IDENTITY_NUC
Gap 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: gb_esc2:
3: gb_esc3:
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5: gb_esc5:
6: gb_esc6:
7: gb_esc7:
8: gb_esc8:
9: gb_esc9:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	57.8	11.6	796	4	BC548055 602575976
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6	54.6	10.9	818	8	AQ895736 HS_5439_A
7	54.6	10.9	979	2	BE740888 601593320
8	54.4	10.9	292	1	A1521806 C182F06.X
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10	53.8	10.8	317	8	ACG75866 Pan t10g1
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13	53.2	10.6	533	5	BX492724 DKFZP781C
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C 29	52	10.4	228	8	AQ316848
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C 38	51.4	10.3	218	1	A1206963
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C 40	51.4	10.3	429	2	AM068007
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ALIGNMENTS

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LOCUS AGENCOURT 14257551 NIH MGC_180 Homo sapiens cDNA clone
DEFINITION IMAGE:30387007 5', mRNA sequence.
ACCESSION CD358047
VERSION CD358047.1 GI:31129458
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1995)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@nci.nih.gov

Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLN at:
http://image.llnl.gov
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Library."

ORIGIN

Query Match 27.8%; Score 138.8; DB 6; Length 995;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)
5019.154 Million cell updates/sec

Title: US-09-982-091a-1_COPY_4200_4740

Perfect score: 541
Sequence: 1 gtaaatcttccatcagaga.....ttcaaaaaaaaaaaaaa 541

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14865122

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:

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6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
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22: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
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25: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	4754	9	US-09-982-091a-1
2	65.6	12.1	8056	20	US-10-473-126-386
3	65.4	12.1	5979	14	US-10-239-676-18
4	65.4	12.1	5979	15	US-10-240-453-26
5	64.6	11.9	8305	15	US-10-311-455-1542
6	62.6	11.6	8056	20	US-10-473-126-240
7	62.4	11.5	461	10	US-09-814-353-17724

Query Match	Score	DB 9	Length	4754
Best Local Similarity	100.0%	Pred. No. 4.1e-88		
Matches 541	Conservative	0	Mismatches	0
Indels	0	Gaps	0	

QY 1 gtaaatcttccatcagagaataccttcaaaatacagtaattgtttcaaac 60
DB 4200 gtaaatcttccatcagagaataccttcaaaatacagtaattgtttcaaac 4259

ALIGNMENTS

RESULT 1
US-09-982-091a-1
Sequence 1, Application US/09982091A
Patent No. US20020151030A1
GENERAL INFORMATION:
APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
APPLICANT: KOMAGAI, AKIO
APPLICANT: DUNPHY, William
TITLE OF INVENTION: CLASPIN PROTEINS AND METHODS OF USE THEREOF
FILE REFERENCE: CIT320-1
CURRENT APPLICATION NUMBER: US/09/982,091A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: US 60/241,246
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 4754
TYPE: DNA
ORGANISM: Xenopus laevis
US-09-982-091a-1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 00:01:51 ; Search time 89.5161 Seconds
(without alignments)
9889.010 Million cell updates/sec

Title: US-09-982-091a-1_COPY_4200_4740

Perfect score: 541

Sequence: 1 gcaaacctcacccatcagaga.....ttcaaaaaaaaaaaaaa 541

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	55	10.2	191569	4	US-09-949-016-15940
4	54.6	10.1	9447	4	US-09-949-016-14649
5	54.4	10.1	47781	4	US-09-949-016-14992
6	54.4	10.1	47781	4	US-09-949-016-14992
7	54.4	10.1	47781	4	US-09-949-016-14992
8	54	10.0	1431	3	US-09-316-083-2
9	54	10.0	1431	4	US-09-933-700-2
10	54	10.0	65415	4	US-09-949-016-16699
11	53.6	9.9	312470	4	US-09-949-016-14043
12	52.8	9.8	636	3	US-08-998-416-1137
13	52.8	9.8	837	3	US-08-998-416-1137
14	52.4	9.7	3350	3	US-08-617-860B-3
15	52.2	9.6	187169	4	US-09-949-016-12776
16	52.2	9.6	191569	4	US-09-949-016-15940
17	52	9.6	50383	4	US-09-949-016-17600
18	51.8	9.6	601	4	US-09-949-016-156535
19	51.8	9.6	615	3	US-08-998-416-186
20	51.8	9.6	231129	4	US-09-949-016-16110
21	51.8	9.6	266293	4	US-09-949-016-11934
22	51.6	9.5	640681	4	US-09-790-988-1
23	51	9.4	601	4	US-09-949-016-30530
24	51	9.4	601	4	US-09-949-016-30531
25	51	9.4	601	4	US-09-949-016-37149
26	51	9.4	601	4	US-09-949-016-37150
27	51	9.4	601	4	US-09-949-016-37163

C 28	51	9.4	601	4	US-09-949-016-37164	Sequence 37164, A
C 29	51	9.4	601	4	US-09-949-016-145867	Sequence 145867, A
C 30	51	9.4	601	4	US-09-949-016-145868	Sequence 145868, A
C 31	51	9.4	601	4	US-09-949-016-146135	Sequence 146135, A
C 32	51	9.4	601	4	US-09-949-016-146136	Sequence 146136, A
C 33	51	9.4	601	4	US-09-949-016-146403	Sequence 146403, A
C 34	51	9.4	601	4	US-09-949-016-146404	Sequence 146404, A
C 35	51	9.4	205044	4	US-09-949-016-15851	Sequence 15851, A
C 36	51	9.4	205044	4	US-09-949-016-15852	Sequence 15852, A
C 37	51	9.4	205044	4	US-09-949-016-15853	Sequence 15853, A
C 38	51	9.4	223471	4	US-09-949-016-12387	Sequence 12387, A
C 39	51	9.4	223471	4	US-09-949-016-12387	Sequence 12387, A
C 40	51	9.4	223471	4	US-09-949-016-12725	Sequence 12725, A
C 41	50.8	9.4	18989	4	US-09-949-016-13435	Sequence 13435, A
C 42	50.8	9.4	21885	4	US-09-949-016-12600	Sequence 12600, A
C 43	50.8	9.4	101128	4	US-09-949-016-14293	Sequence 14293, A
C 44	50.6	9.4	119153	4	US-09-949-016-12378	Sequence 12378, A
C 45	50.4	9.3	19124	2	US-08-487-826B-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhuan
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487, 826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelien, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CPI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13
Query Match 10.9%; Score 58.8; DB 2; Length 19124;
Best Local Similarity 48.8%; Pred. No. 0.0034;

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OM nucleic - nucleic search, using bw model

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Title: US-09-982-091a-1_COPY_4200_4740

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 66479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 4	365.2	67.5	730	5	BP734936 BP734936
C 5	299.4	55.3	921	5	BU906840 AGENCOURT
C 6	160.6	29.7	609	7	CR585851 CR585851
C 7	159	29.4	568	1	AL879187 AL879187
C 8	154.2	28.5	366	5	BX780631 BX780631
C 9	150.6	27.8	737	5	BX783149 BX783149
C 10	148.4	27.4	550	1	AL881003 AL881003
C 11	148	26.2	328	1	AL857987 AL857987
C 12	142	26.2	322	1	AL865252 AL865252
C 13	133.2	24.6	659	1	AL847560 AL847560
C 14	133.2	24.6	659	1	AL847560 AL847560
C 15	77.6	14.3	1101	9	CNS000EV1
C 16	74.6	13.8	1101	9	CNS016L1
C 17	73.8	13.6	928	9	CNS000B01
C 18	72.6	13.6	1092	9	CNS000DKY
C 19	72.6	13.4	1101	9	CNS020K7
C 20	72.2	13.3	1101	9	CNS000B01
C 21	70.8	13.1	885	6	CA973527 CA973527
C 22	70.6	13.0	1101	9	CNS0039G
C 23	69.6	12.9	1203	9	CNS01603
C 24	69.4	12.8	1092	9	CNS020K7

25	68.6	12.7	1001	9	CNS0155H	AL105023 Drosophila
26	68.2	12.6	1101	9	CNS00L72	AL078714 Drosophila
27	68.2	12.6	1225	9	CNS0161D	AL106171 Drosophila
28	67.8	12.5	1101	9	CNS0042W	AL055440 Drosophila
C 29	67.6	12.5	1101	9	CNS0021J	AL061936 Drosophila
C 30	67.6	12.5	1101	9	CNS000E7	AL069440 Drosophila
C 31	67	12.4	1200	9	CNS016CO	AL106578 Drosophila
C 32	66.6	12.3	1200	9	CNS016CO	AL106578 Drosophila
C 33	66.4	12.3	1190	9	CNS020N7	AL106578 Drosophila
C 34	65.4	12.1	866	9	AG515880	AL206208 Tetradon
C 35	65.4	12.1	869	9	CNS01722	AG515880 Mus muscu
C 36	65.4	12.1	935	9	CNS000JKN	AL108680 Drosophila
C 37	65.4	12.1	1663	3	CR652973	AL076398 Drosophila
C 38	65.2	12.1	1101	9	CNS00FVE	CR652973 Tetradon
C 39	65.2	12.1	1780	9	AG320553	AG320553 Mus muscu
40	65	12.0	1101	9	CNS01720	AL108704 Drosophila
41	64.8	12.0	1013	9	CNS06RPQ	AL412260 T7 end of
42	64.2	11.9	660	8	BH183498	BH183498 023 L 07-
43	64.2	11.9	758	9	CNS070N7	AL620449 T3 end of
44	63.8	11.8	926	9	AG547036	AG547036 Mus muscu
C 45	63.8	11.8	926	4	BM358145	BM358145 GA_Ea000

ALIGNMENTS

RESULT 1
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LOCUS BJ055644 NIBB Mochii normalized Xenopus neurula library Xenopus
DEFINITION laevis cDNA clone XLO50a10 3', mRNA sequence.
ACCESSION BJ055644 GI:17468838
VERSION BJ055644.1
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 604)

REFERENCE
AUTHORS Kohayama, A., Terakawa, C., Mochii, M., Ueno, N., Shin-I, T. and Kohayama, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)

TITLE
JOURNAL
COMMENT Contact: Tadao Shin-I
Center For Genetic Resource Information
National Institute of Genetics
111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
The information of this clone is available through the following URL.
http://xenopus.nibb.ac.jp.

FEATURES
source location/Qualifiers
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/organism="Xenopus laevis"
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ORIGIN

Query Match 91.8% Score 496.6; DB 4; Length 604;
Best Local Similarity 98.8% Pred. No. 4.3e-78;
Matches 499; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GTAATCTACCTCATGAGATACAGATACCTTACCAAAATACAGTAATTTGTTTACAAC 60
DB 512 GTAATTTACCTCATGAGATACAGATACCTTACCAAAATACAGTAATTTGTTTACAAC 453

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 21:10:56 : Search time 280.519 Seconds
(without alignments)
11416.644 Million cell updates/sec

Title: US-09-982-091a-1_COPY_4200_4740

Perfect score: 541

Sequence: 1 gtaaatctacccatcagaga.....ttcaaaaaaaaaaaaaa 541

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	65.6	12.1	8056	8 ABZ10246	Abz10246 Haematopo
3	65.4	12.1	5979	4 AAS45313	Aas45313 Chemocall
4	65.4	12.1	5979	6 ABK28152	Abk28152 DNA trans
5	64.6	11.9	8305	6 ABK33569	Abk33569 Human imm
6	62.6	11.6	8056	8 ABZ10100	Abz10100 Haematopo
7	62.4	11.5	461	5 ADL43834	Adl43834 Human ova
8	62.2	11.5	8056	8 ABZ10246	Abz10246 Haematopo
9	61	11.3	14919	4 AAS46506	Aas46506 Tumour su
10	59.2	10.9	6101	6 ABK33475	Abk33475 Human imm
11	59.2	10.9	8056	8 ABZ10100	Abz10100 Haematopo
12	58.8	10.9	6101	6 ABK33474	Abk33474 Human imm
13	58.8	10.9	7851	6 ABK33761	Abk33761 Human imm
14	58.8	10.9	19124	2 AAT72882	Aat72882 Plasmodin
15	58.8	10.9	19124	3 AAZ28287	Aaz28287 Plasmodin
16	58.6	10.8	6056	6 ABK33026	Abk33026 Human imm
17	58.6	10.8	7167	6 ABK32400	Abk32400 Human imm
18	58.4	10.7	380	4 AAI80354	Aai80354 Human pol
19	57.8	10.7	15861	6 ABK32525	Abk32525 Human imm
20	57.4	10.6	6631	6 ABK28339	Abk28339 DNA trans

ALIGNMENTS

21	57.2	10.6	2000	6 ABZ15446	Abz15446 Arabidops
22	57.2	10.6	17280	4 AAS46772	Aas46772 Tumour su
23	56.8	10.5	9810	6 ABK32426	Abk32426 Human imm
24	56.2	10.4	38342	4 AAS46745	Aas46745 Tumour su
25	56.2	10.4	38342	6 ABK31506	Abk31506 Signal tr
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34	55.6	10.3	14919	4 AAS46506	Aas46506 Human gen
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36	55	10.2	28564	10 ADE61172	Ad61172 Human imm
37	55	10.2	28564	10 ADD46006	Add46006 Human gen
38	54.8	10.1	302	5 ADL37732	Adl37732 Human ova
39	54.8	10.1	302	5 ADL37732	Adl37732 Human ova
40	54.8	10.1	7851	6 ABK33760	Abk33760 Human imm
41	54.8	10.1	40324	6 ABK67149	Abk67149 Human ang
42	54.6	10.1	6794	6 ABK31265	Abk31265 Signal tr
43	54.6	10.1	6794	6 ABK31265	Abk31265 Signal tr
44	54.6	10.1	6794	6 AAS61175	Aas61175 Human gen
45	54.4	10.1	727	4 AAI95197	Aai95197 Human neu

RESULT 1	ABK52610	standard; DNA; 4754 BP.
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AC	ABK52610	
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DT	27-AUG-2002	(first entry)
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XX	XX	
KW	Chk1 protein; SQ/TQ motif; Isoelectric point; cell cycle progression;	
KW	nuclear localisation signal; DNA replication checkpoint; benign neoplasm;	
KW	cell proliferative disorder; malignant neoplasm; frog; claspin; gene; ds.	
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PN	W0200233115-A2.	
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PD	25-APR-2002.	
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PF	17-OCT-2001; 2001WO-US032316.	
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PR	17-OCT-2000; 2000US-0241246P.	
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PA	(CALY) CALIFORNIA INST OF TECHNOLOGY.	
PI	Kumagai A, Dunphy WG;	
XX	XX	
DR	WPI; 2002-454610/48.	
XX	XX	
DR	P-PSDB; AAU97586.	
XX	XX	
PT	Novel Claspin polypeptide specifically interacting with chk1 protein	
PT	useful for identifying compound that modulates cell cycle progression and	
PT	for treating cell proliferative disorder like neoplasm.	
XX	XX	
PS	Claim 7; Fig 1; 97p; English.	
XX	XX	
CC	The present invention relates to a new substantially pure Claspin	

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 21:21:46 : Search time 1857.72 Seconds
(without alignments)
14110.995 Million cell updates/sec

Title: US-09-982-091a-1_COPY_4200_4740

Perfect score: 541
Sequence: 1 gtaatcctaccctcctacagaga.....ttaaaaaaaaaaaaaaaaaa 541

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: gb_lm:*
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10: gb_to:*
11: gb_gts:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	68.6	12.7	254436	AE014827	AE014827 Plasmodu
5	68.4	12.6	201254	CR391938	CR391938 Danio rer
6	67.8	12.5	58891	AC021479	AC021479 Mus muscu
7	67.8	12.5	254050	PR929358	PR929358 Plasmodu
8	67.2	12.4	77835	PFMAL13_P2_3	PFMAL13_P2_3
9	67.2	12.4	340552	CR450693	CR450693 Plasmodu
10	66.8	12.3	148484	CR450693	CR450693 Plasmodu
11	66.6	12.3	242140	CR450693	CR450693 Plasmodu
12	66.4	12.3	159618	AC096750	AC096750 Danio rer
13	66.4	12.3	179066	CR450782	CR450782 Danio rer
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15	66.2	12.2	119475	CR318662	CR318662 Danio rer
16	66	12.2	161444	CR318662	CR318662 Danio rer
17	66	12.2	185596	AC021553	AC021553 Homo sapi
18	66	12.2	250029	AE014816	AE014816 Plasmodu
19	65.8	12.2	64707	AC115607	AC115607 Dictyoste

20	65.6	12.1	8056	AX599046	AX599046 Sequence
21	65.6	12.1	27694	HASMT	D31785 Pichia cana
22	65.6	12.1	141946	CR396585	CR396585 Danio rer
23	65.4	12.1	5979	AX277855	AX277855 Sequence
24	65.4	12.1	5979	AX323538	AX323538 Sequence
25	65.4	12.1	152209	HS1108D11	AL034419 Human DNA
26	65.2	12.1	54441	AC115584	AC115584 Dictyoste
27	65.2	12.1	254050	PR929358	AL929358 Plasmodu
28	65	12.0	64707	AC115607	AC115607 Dictyoste
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33	64.8	12.0	191887	CR407563	CR407563 Danio rer
34	64.8	12.0	249995	AE014840	AE014840 Plasmodu
35	64.8	12.0	299050	AP004173	AP004173 Mycoplasm
36	64.6	11.9	8305	AX346471	AX346471 Sequence
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39	64.6	11.9	242140	CR456633	CR456633 Danio rer
40	64.6	11.9	330199	CR456633	CR456633 Danio rer
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ALIGNMENTS

RESULT 1
LOCUS AF297867 4754 bp mRNA linear VRT 28-MAY-2002
DEFINITION Xenopus laevis Claspin mRNA, complete cds.
ACCESSION AF297867
VERSION AF297867.2 GI:21233661

KEYWORDS
SOURCE
ORGANISM
Xenopus laevis (African clawed frog)
Xenopus laevis

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
11090622
2 (bases 1 to 4754)
Kumagai, A. and Dunphy, W.G.
Direct Submision
Submitted (21-AUG-2000) Biology, California Institute of
Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA
3 (bases 1 to 4754)
Kumagai, A. and Dunphy, W.G.
Direct Submision
Submitted (28-MAY-2002) Biology, California Institute of
Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA
Sequence update by submitter
On May 28, 2002 this sequence version replaced gi:10944335.
location/Qualifiers
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AUTHORS
TITLE
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MEDLINE
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11090622
2 (bases 1 to 4754)
Kumagai, A. and Dunphy, W.G.
Direct Submision
Submitted (21-AUG-2000) Biology, California Institute of
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3 (bases 1 to 4754)
Kumagai, A. and Dunphy, W.G.
Direct Submision
Submitted (28-MAY-2002) Biology, California Institute of
Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA
Sequence update by submitter
On May 28, 2002 this sequence version replaced gi:10944335.
location/Qualifiers
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/mol_type="mRNA"
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/db_xref="GI:21233662"

CDS

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OM nucleic - nucleic search, using sw model

Run on: October 4, 2005, 02:35:27 ; Search time 687.831 Seconds
(without alignments)
5019.154 Million cell updates/sec

Title: US-09-982-091A-1_COPY_1_500

Perfect score: 500

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Scoring table:

IDENTITY_NUC
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Searched: 7442561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	47.6	9.5	2859	19 US-10-437-963-57519	Sequence 97519, A
3	46.2	9.2	583	9 US-09-864-761-20772	Sequence 20772, A
4	46.2	9.2	114771	20 US-10-723-860-458	Sequence 4012, Ap
5	44.4	8.9	2717	19 US-10-451-467A-237	Sequence 237, App
7	44.2	8.8	421	10 US-09-803-719-1138	Sequence 1138, App

8	44.2	8.8	496	10 US-09-918-995-21694	Sequence 21694, A
9	44.2	8.8	4756	9 US-09-982-091A-3	Sequence 3, Appli
10	44.2	8.8	4804	20 US-10-357-920-30217	Sequence 30217, A
11	44	8.8	393	10 US-09-803-719-853	Sequence 853, App
12	44	8.8	401	20 US-10-357-930-15892	Sequence 15892, A
13	44	8.8	422	10 US-09-803-719-1139	Sequence 1139, Ap
14	44	8.8	452	20 US-10-357-990-45720	Sequence 45720, A
15	43.8	8.8	387	19 US-10-021-123-941	Sequence 941, App
16	43.6	8.7	344	19 US-10-437-963-5076	Sequence 5076, Ap
17	43.2	8.6	766	9 US-09-864-761-19608	Sequence 19608, A
18	43.2	8.6	1944	9 US-09-864-761-19608	Sequence 2825, Ap
19	42.6	8.5	408	21 US-10-275-323A-13	Sequence 13, Appl
20	42.6	8.5	519	19 US-10-437-963-101926	Sequence 101926
21	42	8.4	408	10 US-09-803-719-777	Sequence 777, App
22	42	8.4	1452	17 US-10-158-057-65	Sequence 65, Appl
23	41.8	8.4	58837	9 US-09-982-091A-5	Sequence 5, Appli
24	41.4	8.3	1083	22 US-10-450-763-12549	Sequence 12549, A
25	41.4	8.3	58985	10 US-09-901-152-3	Sequence 3, Appli
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29	41.2	8.2	327	9 US-09-864-761-28059	Sequence 28059, A
30	41.2	8.2	3585	19 US-10-437-963-62522	Sequence 62522, A
31	41.2	8.2	63693	19 US-10-741-601-5650	Sequence 5650, Ap
32	41	8.2	1284	16 US-10-032-585-6386	Sequence 6386, Ap
33	40.6	8.1	872	9 US-09-925-297-358	Sequence 358, App
34	40.6	8.1	1984	14 US-10-050-704-70	Sequence 70, Appl
35	40.6	8.1	1984	19 US-10-798-512-70	Sequence 70, Appl
36	40.6	8.1	4623	9 US-09-864-864-288	Sequence 288, App
37	40.6	8.1	4633	22 US-10-450-763-5717	Sequence 5717, Ap
38	40.6	8.1	4637	18 US-10-363-616-11	Sequence 11, Appl
39	40.6	8.1	4684	18 US-10-363-616-12	Sequence 12, Appl
40	40.6	8.1	4689	22 US-10-450-763-9626	Sequence 9626, Ap
41	40.6	8.1	5136	22 US-10-450-763-20519	Sequence 20519, A
42	40.4	8.1	456	9 US-09-864-761-11468	Sequence 11468, A
43	40.4	8.1	591	19 US-10-021-323-13554	Sequence 13554, A
44	40.4	8.1	671	14 US-10-184-644-346	Sequence 346, App
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ALIGNMENTS

RESULT 1
US-09-982-091A-1
; Sequence 1, Application US/09982091A
; Patent No. US20020151030A1
GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: KUMAGAI, AKIKO
; APPLICANT: DUNPHY, WILLIAM
; TITLE OF INVENTION: CASPAIN PROTEINS AND METHODS OF USE THEREOF
; FILE REFERENCE: CIT11320-1
; CURRENT APPLICATION NUMBER: US/09/982,091A
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US 60/241,246
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 4754
TYPE: DNA
; ORGANISM: Xenopus laevis
US-09-982-091A-1

Query Match 100.0%; Score 500; DB 9; Length 4754;
Best Local Similarity 100.0%; Pred. No. 9.7e-118;
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ACAGTATAGGCGGCAATTCAGAGCGGAGTGTGCGGAGTGTCTATCACC 60
1 ACAGTATAGGCGGCAATTCAGAGCGGAGTGTGCGGAGTGTCTATCACC 60

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OM nucleic - nucleic search, using sw model

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(without alignments)
9889.010 Million cell updates/sec

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Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

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Total number of hits satisfying chosen parameters: 2405568

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: /cgn2_6/prodata/1/ina/6B COMB. seq.*
- 5: /cgn2_6/prodata/1/ina/PCTUS COMB. seq.*
- 6: /cgn2_6/prodata/1/ina/Backfillseq. seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	43.8	8.8	767677	4	US-09-949-016-17361 Sequence 17361, A
5	43.8	8.6	832	4	US-09-621-976-2813 Sequence 2813, Ap
6	41.8	8.4	53737	4	US-09-949-016-16197 Sequence 16197, A
7	40.6	8.1	642	4	US-09-248-796A-4755 Sequence 4755, Ap
8	40.2	8.0	1832	4	US-09-976-594-537 Sequence 537, App
9	40.2	8.0	1961	4	US-09-976-594-535 Sequence 535, App
10	40.2	8.0	10304	4	US-09-627-465B-11 Sequence 1, Appl
C 11	39.8	8.0	278866	4	US-09-949-016-13922 Sequence 13922, A
C 12	39.8	8.0	278866	4	US-09-949-016-13923 Sequence 13923, A
C 13	39.8	8.0	278866	4	US-09-949-016-13924 Sequence 13924, A
C 14	39.8	8.0	278866	4	US-09-949-016-13925 Sequence 13925, A
C 15	39.8	8.0	278866	4	US-09-949-016-13926 Sequence 13926, A
C 16	39.8	8.0	278866	4	US-09-949-016-14699 Sequence 14699, A
C 17	39.8	8.0	278866	4	US-09-949-016-14700 Sequence 14700, A
C 18	39.8	8.0	278866	4	US-09-949-016-14701 Sequence 14701, A
C 19	39.8	8.0	278866	4	US-09-949-016-14702 Sequence 14702, A
C 20	39.8	8.0	278866	4	US-09-949-016-14703 Sequence 14703, A
21	39.6	7.9	3561	4	US-09-248-796A-2080 Sequence 2080, Ap
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23	39.6	7.8	289	3	US-09-007-005-17 Sequence 17, Appl
24	39.6	7.8	289	3	US-09-244-796-17 Sequence 17, Appl
25	39.6	7.8	2130	4	US-09-248-796A-4942 Sequence 4942, Ap
26	38.8	7.8	1002	4	US-09-248-796A-1249 Sequence 1249, Ap
27	38.6	7.7	1566	4	US-09-248-796A-4899 Sequence 4899, Ap

28	38.6	7.7	192302	4	US-09-949-016-15270 Sequence 15270, A
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31	38	7.6	1284	4	US-09-107-532A-825 Sequence 825, App
32	38	7.6	1596	4	US-09-248-796A-6132 Sequence 6132, Ap
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34	37.8	7.6	906	4	US-09-134-001C-3175 Sequence 3175, Ap
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36	37.8	7.6	1620	4	US-09-710-279-789 Sequence 789, App
37	37.8	7.6	1623	3	US-09-134-001C-1868 Sequence 1868, App
38	37.8	7.6	2295	1	US-08-375-300-3 Sequence 3, Appl1
39	37.8	7.6	2295	3	US-09-177-431-3 Sequence 3, Appl1
40	37.8	7.6	2295	5	PCT-US95-16930-3 Sequence 3, Appl1
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45	37.8	7.6	4080	1	US-08-375-300-1 Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DOMNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZpt-Fls
US-08-232-463-14
Query Match 14.1%; Score 70.6; DB 1; Length 7218;

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 23:18:16 : Search time 1645.02 Seconds
(without alignments)
11569.535 Million cell updates/sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
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8: gb_gatc7.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	459.2	91.8	981	6	CA974658 AGENCOURT
2	447.4	89.5	915	6	CA791641 AGENCOURT
3	432.8	86.6	926	5	BU907710 AGENCOURT
4	400.8	80.2	955	6	CA982465 AGENCOURT
5	286.4	57.3	661	1	AL870060 AL870060
6	282.6	56.5	858	1	AL863727 AL863727
7	278.6	55.7	571	7	CF783399 AGENCOURT
8	278.6	55.7	577	7	CF783398 AGENCOURT
9	273.6	54.7	543	1	AL896540 AL896540
10	273.6	54.7	561	5	BX774034 BX774034
11	273.6	54.7	643	1	AL857528 AL857528
12	246	49.2	631	1	AL850776 AL850776
13	243.4	48.7	649	1	AL863524 AL863524
14	242.8	48.6	634	1	AL873704 AL873704
15	242.8	48.6	656	1	AL866230 AL866230
16	200.6	40.1	933	5	BX756585 BX756585
17	182.4	36.5	663	1	AL891701 AL891701
18	179.8	36.0	553	1	AL866562 AL866562
19	170.4	34.1	864	5	BX783588 BX783588
20	138.4	27.7	494	1	AL874978 AL874978
21	124.6	24.9	608	1	AL881027 AL881027
22	97	19.4	537	1	AL882988 AL882988
23	76.8	15.4	485	1	AL889102 AL889102
24	57	11.4	1101	9	CNS00396

c 25	56.2	11.2	849	8	A2546009	A2546009	ENTFWS3TF
c 26	55.2	11.0	648	2	BE349803	BE349803	hq43C11.x
c 27	53.6	10.7	905	8	A2550256	A2550256	ENTFV58TR
c 28	53	10.6	629	2	BE329068	BE329068	hq36d07.x
c 29	52.6	10.5	509	5	BO599603	BO599603	MI-P-E6-a
c 30	52.6	10.5	630	5	BX665807	BX665807	BP665807
c 31	52.6	10.5	630	5	BX665807	BX665807	BP665807
c 32	52.6	10.5	869	5	BP166258	BP166258	BP166258
c 33	52.4	10.5	843	8	A2551618	A2551618	ENTFV54TR
c 34	52.4	10.5	931	8	A2548467	A2548467	ENTFV54TR
c 35	52.4	10.5	908	8	BH160272	BH160272	ENTFV54TR
c 36	52	10.4	640	2	BE349846	BE349846	hq43C05.x
c 37	51.8	10.4	656	2	BE349729	BE349729	hq43C05.x
c 38	51.4	10.3	976	8	BH149883	BH149883	ENTFV54TR
c 39	51.4	10.3	1490	8	CC293290	CC293290	CH261-62J
c 40	50.8	10.2	888	8	A2528430	A2528430	ENTFV54TR
c 41	48.6	9.7	877	8	A2531291	A2531291	ENTFV54TR
c 42	48.6	9.7	912	8	A2551092	A2551092	ENTFV54TR
c 43	48.4	9.7	507	5	BO739620	BO739620	PFBST08B4
c 44	48.4	9.7	836	9	BX143478	BX143478	Danio rer
c 45	48.4	9.7	900	8	A2549980	A2549980	ENTFV54TR

ALIGNMENTS

RESULT 1
CA974658
LOCUS
DEFINITION AGENCOURT 10748008 Wellcome CRC psk egg Xenopus laevis cDNA clone
IMAGE:6327325.5, mRNA sequence.
CA974658
CA974658.1 GI:27507312

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Xenopus laevis (African clawed frog)

REFERENCE
AUTHORS
TITLE
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ccgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)

JOURNAL
COMMENT
CDNA Library Preparation: N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: XGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM13776 row: 1 column: 14
High quality sequence start: 17
High quality sequence stop: 724.
Location/Qualifiers

FEATURES

source

1. 981
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:6327325"
/issue_type="egg"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Wellcome CRC psk egg"
/note="Vector: pBluescript SK-; Site 1: NotI; Site 2: EcoRI; CDNA were oligo-dT primed and directionally cloned. Library was constructed by N. Garrett, P. Lemaire, A.M. Zorn, and J.B. Gurdon (Wellcome/CRC Institute).
Note: This is a Xenopus Gene Collection (XGC) library."

ORIGIN

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model1

Run on: October 3, 2005, 21:10:56 : Search time 259.259 Seconds
(without alignments)
11416.644 Million cell updates/sec

Title: US-09-982-091A-1_COPY_1_500

Perfect score: 500
Sequence: 1 accgcatgagcgcggaattcc.....agaacatgatagcttgagaga 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn19808:*
2: geneseqn19808:*
3: geneseqn20008:*
4: geneseqn2001a:*
5: geneseqn2001b:*
6: geneseqn2002a:*
7: geneseqn2002b:*
8: geneseqn2003a:*
9: geneseqn2003b:*
10: geneseqn2003c:*
11: geneseqn2003d:*
12: geneseqn2004a:*
13: geneseqn2004b:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500	100.0	4754	6	ABK52610 DNA encod
2	48.4	9.7	1998	3	AAA70212 Plasmid
3	46.2	9.2	583	4	AAI13356 Probe #13
4	46.2	9.2	583	4	ABA68463 Human foe
5	46.2	9.2	583	4	AAI148680 Probe #17
6	46.2	9.2	583	4	ABA50512 Human bre
7	46.2	9.2	583	4	ABA35452 Human bre
8	46.2	9.2	583	4	AAK42604 Human bon
9	46.2	9.2	583	4	AAK16834 Human bra
10	46.2	9.2	583	4	ABA42222 Human liv
11	46.2	9.2	583	5	AAI08992 Probe #89
12	46.2	9.2	583	6	ABSI6657 Human gen
13	46.2	9.2	1959	4	AAI14146 Probe #40
14	46.2	9.2	1959	4	ABAS5872 Human foe
15	46.2	9.2	1959	4	AAI15531 Probe #42
16	46.2	9.2	1959	4	ABA45382 Human bre
17	46.2	9.2	1959	4	ABA25546 Probe #40
18	46.2	9.2	1959	4	AAK29571 Human bon
19	46.2	9.2	1959	4	AAK04090 Human bra
20	46.2	9.2	1959	4	ABS29202 Human liv

21	46.2	9.2	1959	5	AAI03994	AAI03994 Probe #39
22	46.2	9.2	1959	6	ABS04127	ABS04127 Human gen
23	46.2	9.2	114771	12	ADQ17641	ADQ17641 Human sof
24	44.4	8.9	2717	6	ABQ76406	ABQ76406 S. cerevi
25	44.4	8.9	231004	12	ADQ97855	ADQ97855 Mouse can
26	44.2	8.8	421	4	AAI38080	AAI38080 Novel hum
27	44.2	8.8	496	9	ACH34482	ACH34482 Human end
28	44.2	8.8	4414	10	ADC30694	ADC30694 Human nov
29	44.2	8.8	4755	6	ABK52611	ABK52611 DNA encod
30	44.2	8.8	4804	5	ABV30199	ABV30199 Human pro
31	44	8.8	393	4	AAI37795	AAI37795 Novel hum
32	44	8.8	401	5	ABV15901	ABV15901 Human pro
33	44	8.8	406	5	AAI66639	AAI66639 Novel hum
34	44	8.8	411	5	AAI66638	AAI66638 Novel hum
35	44	8.8	422	4	AAI38081	AAI38081 Novel hum
36	44	8.8	452	5	ABV45701	ABV45701 Human pro
37	43.8	8.8	387	13	ACN46160	ACN46160 Cotton pr
38	43.2	8.6	766	4	AAI22114	AAI22114 Probe #12
39	43.2	8.6	766	4	ABA67193	ABA67193 Human foe
40	43.2	8.6	766	4	AAI47409	AAI47409 Probe #16
41	43.2	8.6	766	4	ABA49279	ABA49279 Human bre
42	43.2	8.6	766	4	ABA34288	ABA34288 Probe #12
43	43.2	8.6	766	5	AAI07812	AAI07812 Probe #78
44	43.2	8.6	1299	3	AAI70111	AAI70111 Plasmid
45	43.2	8.6	1944	4	AAI12874	AAI12874 Probe #28

ALIGNMENTS

RESULT 1	ABK52610	standard; DNA; 4754 BP.
ID	ABK52610	
XX	ABK52610;	
AC	ABK52610;	
DT	27-AUG-2002	(first entry)
XX		
DE	DNA encoding Xenopus Claspin protein.	
XX		
KW	CHK1 protein; SQ/TQ motif; isoelectric point; cell cycle progression;	
KW	nuclear localization signal; DNA replication checkpoint; benign neoplasm;	
KW	cell proliferative disorder; malignant neoplasm; frog; claspin; gene; ds.	
XX		
OS	Xenopus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	71..3928
FT		/*tag= a
FT		/product= "Xenopus Claspin protein"
PN	W0200233115-A2.	
XX		
PD	25-APR-2002.	
XX		
PF	17-OCT-2001; 2001WO-US032316.	
XX		
PR	17-OCT-2000; 2000US-0241246P.	
XX		
PA	(CALY) CALIFORNIA INST OF TECHNOLOGY.	
XX		
PI	Kumagai A, Dunphy WC;	
XX		
DR	WPI: 2002-454610/48.	
XX		
DR	P-PSDB; AAU97586.	
XX		
PT	Novel Claspin polypeptide specifically interacting with chk1 protein	
PT	useful for identifying compound that modulates cell cycle progression and	
PT	for treating cell proliferative disorder like neoplasm.	
XX		
PS	Claim 7; Fig 1; 97pp; English.	
XX		
CC	The present invention relates to a new substantially pure Claspin	

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OM nucleic - nucleic search, using sw model

Run on: October 3, 2005, 21:21:46 ; Search time 1716.93 seconds
(without alignments)
14110.995 Million cell updates/sec

Title: US-09-982-091a-1_COPY_1_500

Perfect score: 500
Sequence: 1 aagcatatggcgccgaattcc.....agaacatgatgctcgaga 500

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sbs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	500	100.0	4754	5 AF297867	AF297867 Xenopus 1
2	273.6	54.7	1044	5 CR761574	CR761574 Xenopus t
3	70.6	14.1	7218	6 I66494	I66494 Sequence 14
4	64.8	13.0	110000	2 PFMAL13_24	Continuation (25 o
5	56.4	11.3	164399	3 PFMAL13p6	298551 Plasmodiu
6	54.8	11.0	151341	5 AL929536	AL929536 zebrafish
7	54.8	11.0	158633	2 BX927349	BX927349 Danio rer
8	54.4	10.9	794	5 BX935928	BX935928 Gallus ga
9	53.6	10.7	1211	10 RATSBP	J02675 Rat prostat
10	53.2	10.6	143342	2 CR388191	CR388191 Danio rer
11	53.2	10.6	347582	3 PFMAL4p1	AL034557 Plasmodiu
12	52	10.4	110000	2 PFMAL13_07	Continuation (8 of
13	52	10.4	250589	2 AC130135	AC130139 Rattus no
14	51.6	10.3	347050	3 PFA929351	AL929351 Plasmodiu
15	51.4	10.3	110000	2 PFMAL7p1_09	Continuation (10 o
16	51.4	10.3	205429	2 AC005506	AC005506 Plasmodiu
17	51.4	10.3	253132	3 AE014846	AE014846 Plasmodiu
18	51	10.2	110000	2 PFMAL7p1_11	Continuation (12 o
19	51	10.2	110000	2 PFMAL8p1_02	Continuation (3 of

20	50.8	10.2	61052	2 AC123513	AC123513 Dictyoste
21	50.8	10.2	115758	3 AC104634	AC104634 Homo sapi
22	50.8	10.2	136240	3 AC117070	AC117070 Dictyoste
23	50.4	10.1	250823	3 AE014821	AE014821 Plasmodiu
24	50.4	10.1	251448	3 AE014819	AE014819 Plasmodiu
25	50.4	10.1	254050	3 PFA929358	AL929358 Plasmodiu
26	50	10.0	158548	3 PFMAL3p2	AL034558 Plasmodiu
27	50	10.0	250029	3 PFMAL4p3	AE014838 Plasmodiu
28	49.8	10.0	34347	2 BX957360	BX957360 Danio rer
29	49.8	10.0	124801	2 AC149906	AC149906 Strongylo
30	49.8	10.0	199698	2 BX004991	BX004991 Danio rer
31	49.8	10.0	215313	2 AC100791	AC100791 Homo sapi
32	49.4	9.9	72383	2 AC027746	AC027746 Homo sapi
33	49.4	9.9	164347	2 AC104805	AC104805 Homo sapi
34	49.2	9.8	974	3 PFA929352	AL929352 Plasmodiu
35	48.8	9.8	418	3 BC062215	BC062215 Homo sapi
36	48.8	9.8	115990	5 BX890614	BX890614 zebrafish
37	48.4	9.7	3016	3 PFA929352	AL929352 Plasmodiu
38	48.4	9.7	16010	3 AE001410	AE001410 Plasmodiu
39	48.4	9.7	175127	2 AC016048	AC016048 Homo sapi
40	48.4	9.7	186147	2 CR626891	CR626891 Danio rer
41	48.4	9.7	194969	2 CR847853	CR847853 Danio rer
42	48.2	9.7	250022	3 AE014824	AE014824 Plasmodiu
43	48.2	9.6	96249	9 AC116612	AC116612 Homo sapi
44	47.8	9.6	94534	5 AL929250	AL929250 zebrafish
45	47.8	9.6	313050	3 PFA929352	AL929352 Plasmodiu

ALIGNMENTS

RESULT 1	AF297867	4754 bp	mRNA	linear	VRT 28-MAY-2002
LOCUS	AF297867				
DEFINITION	Xenopus laevis Claspin mRNA, complete cds.				
ACCESSION	AF297867				
VERSION	AF297867.2	GI:21233661			
KEYWORDS					
SOURCE					
ORGANISM	Xenopus laevis (African clawed frog)				
REFERENCE					
AUTHORS	Kumagai, A. and Dunphy, W.G.				
TITLE	Claspin, a novel protein required for the activation of Chk1 during a DNA replication checkpoint response in Xenopus egg extracts				
JOURNAL	Mol. Cell 6 (4), 839-849 (2000)				
MEDLINE	21000493				
PUBMED	11090622				
REFERENCE	2 (bases 1 to 4754)				
AUTHORS	Kumagai, A. and Dunphy, W.G.				
TITLE	Direct Submision				
JOURNAL	Submitted (21-AUG-2000) Biology, California Institute of Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA				
REMARK	3 (bases 1 to 4754)				
COMMENT	Kumagai, A. and Dunphy, W.G.				
FEATURES	Submitted (28-MAY-2002) Biology, California Institute of Technology, 1200 E. California Blvd., Pasadena, CA 91125, USA				
source	Sequence update by submitter				
	On May 28, 2002 this sequence version replaced gi:10944335.				
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	/mol_type="mRNA"				
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	71..3928				
	/notes="required for the activation of Chk1"				
	/codon_start=1				
	/product="Claspin"				
	/protein_id="AA024516.2"				
	/db_xref="GI:21233662"				